The Impact of Covid-19 Pandemic on the Incidence of Tuberculosis

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Abstract. During the outbreak of Covid-19, data showed that the mortality and infection rates of tuberculosis (TB) rose for the first time in nearly a decade. Through the registration data of tuberculosis before and after the COVID-19 outbreak in the United States, this article will predict and assess whether the novel coronavirus will have some impact on the prevalence of tuberculosis, and whether the impact of tuberculosis will increase as the pandemic progresses. This will aid government to take certain measures to approach tuberculosis during the outbreak. Through ARIMA modeling and prediction of TB case numbers with STATA, this study concluded that COVID-19 increases the prevalence of TB, and with the pandemic progressing, the more severe the situation of COVID-19 is, the more cases of TB there are. The innovation of this article is to use STATA software to analyze the impact of novel coronavirus on tuberculosis and offer suggestions for reducing the prevalence of tuberculosis amidst the epidemic. Residents should wear masks more often to prevent airborne transmission of Mycobacterium tuberculosis. Meanwhile, government should improve the identification and diagnosis of mycobacterium tuberculosis medical technology to reduce the incidence rate from the source.

Keywords: Tuberculosis, COVID-19, Novel Coronavirus Pneumonia, STATA, forecast.

1. Introduction

Being an infectious disease caused by the Mycobacterium tuberculosis complex, Tuberculosis can damage organs like the lungs, lymph and kidneys [1]. Patients will generally have dry cough, fatigue, night sweats and other symptoms [2]. TB is indeed one of the top infectious disease killers. With 1.3 million deaths worldwide in 2022, TB ranks 13th among all causes of death [3]. Tuberculosis is mainly transmitted through the air, whose patients make the combined mycobacteria spread to the air through coughing, spitting and other ways [4]. The key current measures to reduce TB transmission are in the identification and treatment of close contacts of recent infections. However, it is challenging to diagnose Mycobacterium tuberculosis, which cannot be directly diagnosed, but only by the indirect detection of the host's immune response to the infection. About one in every four people worldwide harbor Mycobacterium tuberculosis within their body, but only 5% to 10% of those infected develop TB, and most people are in a state of latent TB infection [3, 5]. Hence, it is rather inefficient to reduce Mycobacterium tuberculosis transmission with current strategies, like identification and treatment methods, leaving no effective way in the world to fully control TB.

The COVID-19 outbreak was first discovered in Rhode Island on April 26, 2019. The U.S. authorities announced the first official confirmed case on January 20, 2020, which was followed by the outbreak of COVID-19 there in March 2020.

Before COVID-19 took center stage, tuberculosis was prevalent worldwide and claimed millions of lives. However, through some effective measures, its mortality and incidence rates gradually declined. But during the COVID-19 period, the mortality rate and prevalence of TB rose for the first time in nearly a decade. According to statistics, there were 1.4 million people dying from TB worldwide in 2019, and this number increased to 1.6 million in 2021.To end tuberculosis, humans have made much effort and already achieved the goal of reducing tuberculosis mortality by 35%. Unfortunately, this progress was reversed by COVID-19 [6].

With the registration data of tuberculosis before and after the COVID-19 epidemic in the United States, this article will forecast and determine whether the novel coronavirus will have some impact

on the prevalence of tuberculosis, and whether the impact of tuberculosis will increase as the pandemic progresses. This will aid government to take certain measures to approach tuberculosis during the outbreak.

2. Literature review

In the past, the three coronaviruses were regularly crossed with animals such as bats and then spread to humans, leading to continuous outbreaks and increases of influenza. Previously, viral zoonotic pathogens included the Middle East respiratory syndrome coronavirus (MERS-CoV) and the severe acute respiratory syndrome coronavirus (SARS-CoV) [7]. These viruses, originating in animals, pose a continuous threat to human health. SARS-CoV-2, a novel coronavirus (causing COVID-19), has rapidly spread since its advent in Wuhan, China in December 2019. This virus involves a higher infection rate, a wider impact range, faster transmission speed and severer symptoms, attracting worldwide attention [8].

COVID-19 is a disease caused by novel coronavirus, with common symptoms in patients such as dry cough and shortness of breath. Some may also experience other symptoms, such as headache, sore throat, diarrhea, etc. At the early stage of the infection, symptoms can be mild or even asymptomatic, but all patients display new lung signs. Mild cases typically have sore throat, dry cough, fever, and so on, without severe symptoms or complications. But serious cases can suffer from lung infections, tissue and organ damage and even death. Research shows that 81% of the patients were mild cases, and only a small number of the patients were seriously ill or even fatal. Therefore, the virus has a very serious impact on humans [7].

In response to the spread of COVID-19, many countries have taken corresponding measures. For individuals, people wear masks, wash hand frequently, and avoid going to crowded places [9]. Meanwhile, some governments have enforced mandatory quarantines and lockdowns of severely affected areas with a heavy hand. As a result, many infectious diseases are affected. According to statistics, the epidemics mainly caused by 27 droplets or contact-transmitted pathogens have decreased, including Scarlet Fever, Whooping Cough and Hand, Foot and Mouth Disease. Therefore, the transmission of Mycobacterium tuberculosis has also affected by COVID-19, making its transmission rate decrease [10].

COVID-19 and TB, both classified as airborne respiratory illnesses, damage lung immune regulation, leading to a decrease in immune cells such as upper respiratory tract infections, white blood cells, and lymphocytes during the stage of infection [7]. This results in a double risk of increasing COVID-19 severity and promoting the progression of TB. So, people with latent TB infection may be affected by COVID-19 and are more likely to develop active TB.

Therefore, this article can further determine whether the number of tuberculosis patients is indeed affected during the outbreak. If it is affected, further analysis can be conducted on whether COVID-19 is an important factor affecting tuberculosis. This can provide assistance in preventing the rise of tuberculosis during the arrival of the next influenza virus.

3. Research design

3.1. Data source

To analyze the trend of TB cases in the US from January 2016 to December 2020, data on the number of TB cases was gained from the the US Centers for Disease Control and Prevention (CDC). STATA software was used to extract the time series from January 2016 to February 2020 (tuberculosis data before the outbreak of COVID-19), and then to conduct data analysis and modelling of the sequence.

3.2. Unit root inspection

First, the time series before the new coronavirus outbreak is taken as the logarithm to reduce the heteroscedasticity and obtain new and more stable sequences. Then before modeling, unit root tests need to be performed on the time series and its differences to determine whether these datasets are stable. The unit root test is mainly to test whether the time series has unit root. A sequence with unit root is unstable sequence, while one without it is stable. The variance and mean of a stable time series are fixed, and the existence of the unit root will make the variance and mean of the time series larger over time, making many statistical effects disappear. Therefore, this part should conduct the unit root test. The ADF test is a type of unit root test, and its model formula is as follows:

$$\Delta Y_t = \alpha + \beta Y_{t-1} + \sum_{i=1}^{p} \gamma_i \Delta Y_{t-i} + \varepsilon_t \quad (1)$$

ΔRepresents the first order difference, ε_t is the error term. If the sequence is stationary, then β=0; if the sequence is not stationary, then β=1. For ADF detection with STATA, the table conveys that the p-value of the time series and its first and second differences are 0, much less than 0.1. A null hypothesis stating that there exists a unit root is formulated. If this hypothesis is rejected, it implies that the time series is stable. Hence these data can then be used in the ARIMA model (Table 1).

Table 1. Test of unit roots

	t	p
Ln value	-5.828	0.0000
1st order difference	-7.939	0.0000
2nd order difference	-10.051	0.0000

3.3. ARIMA model setting

The ARIMA model, called Autoregressive Integrated Moving Average Model, weaves together the three components: a Moving Average Model (MA), an Autoregressive Model (AR), and a difference (I). This model uses the data itself to unveil the future data, finds the hidden time series pattern through the autocorrelation and differencing, and then employs the pattern to predict the future.

The ARIMA (p, d, q) model is an approach to forecasting time series with three key elements p, d and q. “p” refers to the autoregressive part, “d” represents the order of the difference, and “q” symbolizes the sliding average part.

The autoregressive section shows the lag value of the model based on the observations, and its starting point of the observations is a linear combination of the previous p periods. Its model formula can be written as follows:

$$AR: Y_t = c + \varphi_1 Y_{t-1} + \varphi_2 Y_{t-2} + \cdots \varphi_p Y_{t-p} + \delta \quad (2)$$

φ in this formula is the model parameter, c is the constant, and δ is the white noise. The order p in this equation determines the number of retrospective observations of the model.

The sliding average section illustrates the lagged values of the error terms used by the model, which aims to establish a relationship between current values and past white noise. Its model formula is as follows:

$$MA: Y_t = \mu + \varepsilon_t + \theta_1 \varepsilon_{t-1} + \theta_2 \varepsilon_{t-2} + \cdots \theta_q \varepsilon_{t-q} \quad (3)$$

θ is the model parameter, $\varepsilon_{t-1}\varepsilon_{t-2}, \varepsilon_{t-q}$ are the past white noises, ε_t is the current white noise, and μ is a constant. The order of this equation, q, determines the number of retrospective white noises of the model.

D is the order of the difference, and when d=n, it indicates that n lag operations have been applied to make the data stationary.

4. The empirical results and analysis

4.1. Model Order Determination

The ARIMA model order can be determined with the autocorrelation function (ACF) and partial autocorrelation function (PACF). ACF indicates the correlation between the observed value and the lagged version, and PACF plots the direct correlation between the observed value and the lagged version. The orders of AR and MA are determined by observing the censoring and trailing of the PACF and ACF plots. Finally, STATA plots PACF and ACF graphs for first-order and second-order differences of the time series.

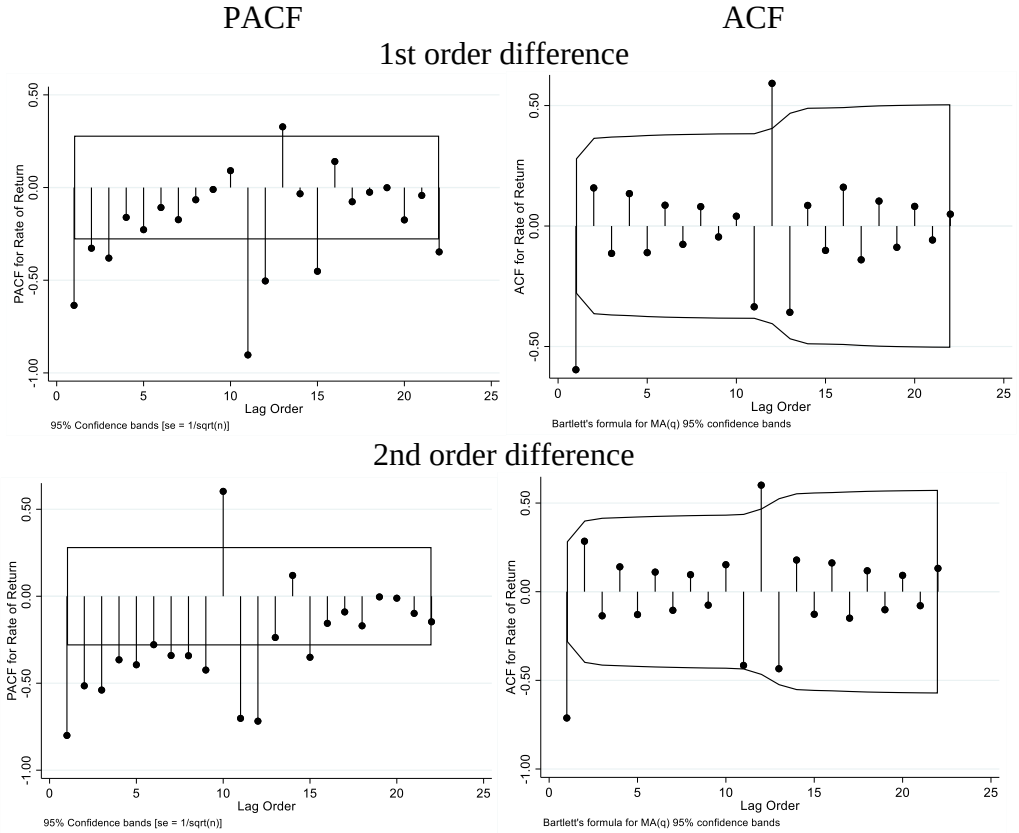

Figure 1. ARMA (p, q) identification (Photo credit: Original)

According to the figure 1, this paper can establish ARIMA (11, 1, 12) and ARIMA (10, 2, 1) models. Since the parameters of ARIMA (11, 1, 12) are too large for MLE to compute, it is excluded. So this part use the ARIMA (10, 2, 1) model.

4.2. Prediction results and interpretation

The ARIMA (10, 2, 1) model predicts the data from March 2020 to December 2020 through the STATA software. AS is shown in Figure 2, the red line is the predicted value while the blue line is the actual value.

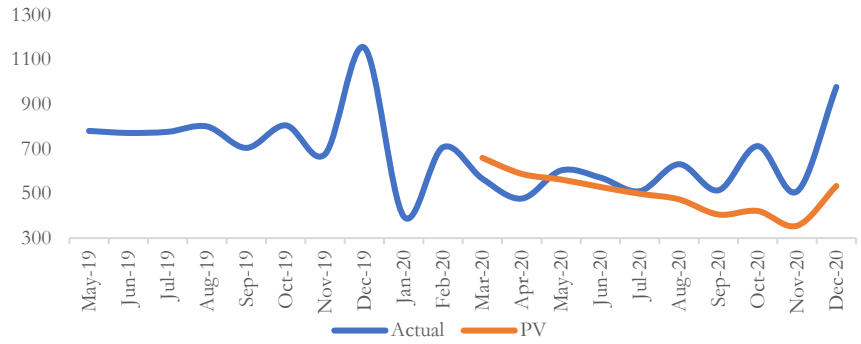

Figure 2. Line plot of predicted and actual numbers of TB (Photo credit: Original)

A graph of the Difference for all prediction results is shown in the figure 2.

Table 2. Predicted and Actual Number of TB and Difference

	Actual	PV	Difference	Difference (%)
May 19th	780			
Jun 19th	771			
Jul 19th	776			
Aug 19th	800			
Sep 19th	704			
Oct 19th	805			
Nov 19th	676			
Dec 19th	1153			
Jan 20th	397			
Feb 20th	707			
Mar 20th	566	659.61361	-93.61361	-14.19%
Apr 20th	477	587.80119	-110.80119	-18.85%
May 20th	603	562.37212	40.62788	7.22%
Jun 20th	571	529.0269	41.9731	7.93%
Jul 20th	510	498.6509	11.3491	2.28%
Aug 20th	631	473.44639	157.55361	33.28%
Sep 20th	514	405.49399	108.50601	26.76%
Oct 20th	712	421.46548	290.53452	68.93%
Nov 20th	509	355.32061	153.67939	43.25%
Dec 20th	977	533.50737	443.49263	83.13%

Note: $Difference$ (%) = ($Actual\ value - predicted\ value$)/$predicted\ value$*100%

According to the figure 3 and table 2, With time going on, difference (%) fluctuates. During the COVID-19 period, in order to prevent the spread of the virus, more people chose to wear masks and avoid crowded places. The transmission route of TB bacteria is blocked, and the number of people suffering from tuberculosis should decline. So the potential reason for this outcome may be that individuals with COVID-19 are more likely to develop tuberculosis, as both diseases mainly affect the lungs and can be transmitted through air. As the number of people with the COVID increases over time, if TB is indeed affected by the COVID-19 virus, the number of cases should be more than expected difference (%) will be bigger and bigger. This is exactly what the line chart in Figure 3 displays, further indicating the impact of COVID-19 on tuberculosis. So it can be concluded that COVID-19 has contributed to a rise in TB cases, and as the epidemic goes on, the more tuberculosis is affected by COVID-19, the more cases of TB there are.

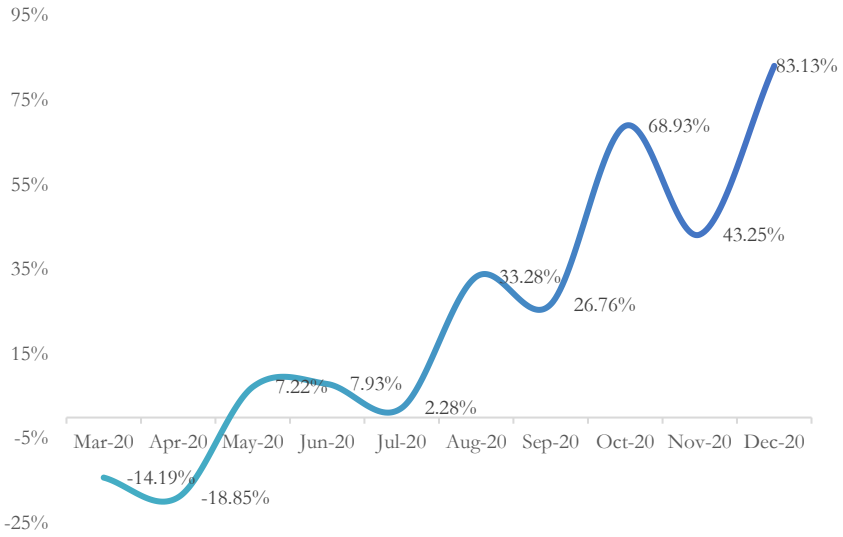

Figure 3. Line Graph of Difference (Photo credit: Original)

5. Discussion

Experimental data have suggested that tuberculosis can be affected by the COVID-19 virus. The COVID-19 virus, known to target the respiratory system, has been found to activate both the adaptability and innate immune response of the human body. An effective immune response helps to clear the COVID-19 virus, but uncontrolled immune reactions can lead to local and systemic tissue loss, reducing the body's immunity and making it more vulnerable to other diseases. COVID-19 is mainly a respiratory disease, where acute disease causes significant damage to the lung and respiratory tract through the replication of novel coronavirus in endothelial cells. However, tuberculosis, a pulmonary infectious disease caused by Mycobacterium tuberculosis, mainly occurs in the lungs. Therefore, lung damage caused by COVID-19 has reduced the patient's immunity to the combined mycobacteria and increased the incidence rate [11].

Tuberculosis is primarily spread through the air, with patients releasing the combined mycobacteria into the atmosphere via coughing, spitting and other ways. The same is true of COVID-19, which is also transmitted through respiratory activities such as breathing, speaking and coughing. Therefore, during the outbreak, the government should encourage mask-wearing to prevent the spread of both viruses. For TB patients, it is even more necessary to wear masks to reduce the spread of combined mycobacteria into the air. Frankly, about one in every four people worldwide harbor Mycobacterium tuberculosis within their body with most of them in a latent tuberculosis infection state. Therefore, these latent patients are inclined to decreased immunity and developing tuberculosis when encountering coronavirus infection. These latent tuberculosis patients are usually asymptomatic and are unaware that they are in a latent state. Therefore, to fundamentally reduce the impact of viruses such as coronavirus on tuberculosis, it is necessary to have more advanced technology to directly diagnose and identify Mycobacterium tuberculosis, or to have stronger medical technology to treat and eliminate Mycobacterium tuberculosis.

6. Conclusion

Tuberculosis is indeed one of the top infectious disease killers, and currently, there is no good effective way to fully control tuberculosis. COVID-19, caused by the novel coronavirus, has a high prevalence. With its wide- range, rapid transmission and severe symptoms, COVID-19 has captured the attention of the world. During the COVID-19 period, the mortality rate and prevalence of TB rose for the first time in nearly a decade. Therefore, this article studies whether COVID-19 has a certain impact on tuberculosis and proposes some measures.

This article predicts the number of TB cases during the outbreak with the STATA software. Through unit root tests and ARIMA model settings, it successfully predicted the number of TB during COVID-19 and compared it with the actual number. It was concluded that COVID-19 has contributed to a rise in TB cases, and as the epidemic goes on, the more TB is affected by COVID-19, the more cases of TB there are.

Since both the novel coronavirus and Mycobacterium tuberculosis are mainly transmitted through the air, this article suggests that the government should call on people to wear masks more frequently. Additionally, improving the identification and diagnostic techniques for tuberculosis according to current medical technology is the fundamental factor to reduce the impact of infectious viruses like the coronavirus on tuberculosis.

The innovation of this article is to use STATA software to analyze the impact of the novel coronavirus on tuberculosis. The limitation is that multiple models are not used, and future research can emphasize more on diagnostic techniques for tuberculosis.

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